SEQUENCE LISTING

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<110> BOUGERET, CECILE
      ZARZOV, PATRICK
      BRIAND, JEAN-FRANCOIS
      THOMAS, DOMINIQUE
<120> METHOD FOR SCREENING AGENTS MODULATING I-KAPPA B-ALPHA
      PROTEIN UBIQUITINATION AND MEANS FOR CARRYING OUT SAID
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<130> 0510-1149
<140> 10/592,944
<141> 2006-09-15
<150> PCT/FR05/050165
<151> 2005-03-15
<150> FR 04 50528
<151> 2004-03-16
<160> 26
<170> PatentIn Ver. 3.3
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gtcactactt tcggttatgg tgttcaatgt tttgctagat acccagatca tatgaaacaa 240
catgactttt tcaagtctgc catgccagaa ggttatgttc aagaaagaac tattttttc 300
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aatagaatcg aattaaaagg tattgatttt aaagaagatg gtaacatttt aggtcacaaa 420
ttggaataca actataactc tcacaatgtt tacatcatgg ctgacaaaca aaagaatggt 480
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cattatcaac aaaatactcc aattggtgat ggtccagtct tgttaccaga caaccattac 600
ttatccactc aatctgcctt atccaaagat ccaaacgaaa agagagacca catggtcttg 660
ttagaatttg ttactgctgc tggtattacc catggtatgg atgaattgta caaactgcag 720
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gagcgccccc aggagtgggc catggagggc ccccgcgacg ggctgaagaa ggagcggcta 840
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<212> PRT

<213> Artificial Sequence

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60

Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser 195 200 205

- Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val 210 215 220
- Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Gln 225 230 235 240
- Ser Pro Pro Pro Lys Lys Lys Arg Lys Val Glu Leu Gly Gly Ser Met 245 250 255
- Phe Gln Ala Ala Glu Arg Pro Gln Glu Trp Ala Met Glu Gly Pro Arg 260 265 270
- Asp Gly Leu Lys Lys Glu Arg Leu Leu Asp Asp Arg His Asp Ser Gly 275 280 285
- Leu Asp Ser Met Lys Asp Glu Glu Tyr Glu Gln Met Val Lys Glu Leu 290 295 300
- Gln Glu Ile Arg Leu Glu Pro Gln Glu Val Pro Arg Gly Ser Glu Pro 305 310 315 320
- Trp Lys Gln Gln Leu Thr Glu Asp Gly Asp Ser Phe Leu His Leu Ala 325 330 335
- Ile Ile His Glu Glu Lys Ala Leu Thr Met Glu Val Ile Arg Gln Val 340 345 350
- Lys Gly Asp Leu Ala Phe Leu Asn Phe Gln Asn Asn Leu Gln Gln Thr 355 360 365
- Pro Leu His Leu Ala Val Ile Thr Asn Gln Pro Glu Ile Ala Glu Ala 370 375 380
- Leu Leu Gly Ala Gly Cys Asp Pro Glu Leu Arg Asp Phe Arg Gly Asn 385 390 395 400
- Thr Pro Leu His Leu Ala Cys Glu Gln Gly Cys Leu Ala Ser Val Gly
 405 410 415
- Val Leu Thr Gln Ser Cys Thr Thr Pro His Leu His Ser Ile Leu Lys 420 425 430
- Ala Thr Asn Tyr Asn Gly His Thr Cys Leu His Leu Ala Ser Ile His 435 440 445
- Gly Tyr Leu Gly Ile Val Glu Leu Leu Val Ser Leu Gly Ala Asp Val 450 455 460
- Asn Ala Gln Glu Pro Cys Asn Gly Arg Thr Ala Leu His Leu Ala Val 465 470 475 480
- Asp Leu Gln Asn Pro Asp Leu Val Ser Leu Leu Leu Lys Cys Gly Ala 485 490 495
- Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln Leu Thr 500 505 510

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<211> 2583

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic construct

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic construct

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 60

Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro 180 185 190

- Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser 195 200 205
- Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val 210 215 220
- Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Gln 225 230 235 240
- Ser Pro Pro Pro Lys Lys Lys Arg Lys Val Glu Leu Gly Gly Ser Met 245 250 255
- Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys Phe Met Cys 260 265 270
- Ser Met Pro Arg Ser Leu Trp Leu Gly Cys Ser Ser Leu Ala Asp Ser 275 280 285
- Met Pro Ser Leu Arg Cys Leu Tyr Asn Pro Gly Thr Gly Ala Leu Thr 290 295 300
- Ala Phe Gln Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro 305 310 315 320
- Pro Arg Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn 325 330 335
- Ser Cys Ala Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser 340 350
- Thr Ala Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn 355 360 365
- Gly Thr Ser Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser 370 380
- Tyr Glu Lys Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser 385 390 395
- Glu Ser Asp Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys 405 410 415
- His Tyr Gln His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln 420 425 430
- Arg Asp Phe Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala 435 440445
- Glu Asn Ile Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu 450 455 460
- Leu Val Cys Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp 465 470 475 480
- Lys Lys Leu Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly 485 490 495

- Leu Ala Glu Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro
 500 505 510
- Pro Asp Gly Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro 515 520 525
- Lys Ile Ile Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly 530 540
- Arg His Ser Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly 545 550 555 560
- Val Tyr Cys Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg
 565 570 575
- Asp Asn Thr Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg
 580 585 590
- Ile Leu Thr Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu
 595 600 605
- Arg Val Ile Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp 610 620
- Val Asn Thr Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala 625 630 635 640
- Val Leu His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys 645 650 655
- Asp Arg Ser Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr 660 665 670
- Leu Arg Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp 675 680 685
- Phe Asp Asp Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys 690 695 700
- Val Trp Asn Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His 705 710 715 720
- Lys Arg Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser 725 730 735
- Gly Ser Ser Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala
 740 745 750
- Cys Leu Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg 755 760 765
- Phe Asp Asn Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys 770 780
- Val Trp Asp Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr 785 790 795 800

Leu Cys Leu Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu 805 810 Gln Phe Asp Glu Phe Gln Ile Val Ser Ser His Asp Asp Thr Ile 825 Leu Ile Trp Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg Ser Pro Ser Arg Thr Tyr Thr Tyr Ile Ser Arg 855 <210> 5 <211> 21 <212> DNA <213> Simian virus 40 <400> 5 21 ccaaaaaaga agagaaaggt c <210> 6 <211> 35 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic primer <400> 6 35 gctgggtacc ttaataatca tattacatgg catta <210> 7 <211> 34 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic primer <400> 7 34 ggcggaattc tatagttttt tctccttgac gtta <210> 8 <211> 35 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic primer

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Asp Tyr Lys Asp Asp Asp Lys
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<212> PRT
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<223> Description of Artificial Sequence: Synthetic
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<400> 19
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                                     10
Tyr Lys Asp Asp Asp Lys
             20
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<211> 16
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Leu Asp. Thr
<210> 23
<211> 74
<212> PRT
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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg
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